## <u>nagrace merin</u>

### FIG. 1A

GGCTGCCGG TGCGGCGGGGTGGAAGCCTCGAGCAGCCGGGGGGGGGG	CCCA	-1 Arg AGG	30 Asp GAC	90 Ile ATC	60 Ser TCC
SCTG -	CTGC	Glu GAG	Ala GCA	Leu	Val GTA
9 9	CCCA	Leu	Lys		
GCAG	rggc	Asp Asp Leu Glu Arg GAC GAT CTG GAG AGG	Glu Gly Lys Ala Asp GAA GGG AAG GCA GAC	Thr	Cys Met Ala TGC ATG GCT
TCGA	CCAG	Asp GAC	Glu GAA	Leu Thr Leu CTC ACC CTC	Cys TGC
AGCC	GGCTTGAAGAGCCGTGCCACCCAGTGGCCCCACTGCCCCA	Leu Ser Trp Tyr Asp CTG TCC TGG TAC GAT	Gly Ser GGG TCA	40 Met Leu ATG CTG	Val GTG
TGGA	CGTG	Tyr	G1y GGG	Met ATG	Leu Val CTG GTG
GAGC	GAGC	Trp		Ala GCC	Val GTG
ງງງງ	TGAA	Ser	Pro Phe Asn CCC TTC AAT	Tyr TAT	Asn Val AAT-GTG
TGCG	CCCT	Leu	Pro	Tyr Tyr TAC TAT	G1y GGC
TGGA	ATAT	Asn AAC	20 Arg CGG	Asn	50 Phe TTT
TGCG	CGCC,	Leu	Ser AGC	Tyr TAC	Val
ອວວອ	9995	Pro	Trp TGG	His	Ile
AGGGGGCCGTGCA	CTGGCCCCGTAT	Asp GAT	Asn AAC	Pro	Ile ATC
AGG	CTG	Met ATG	Gln	Arg AGG	Phe TTT
and the second second			*	*	•

*					* * .	
Ser		270 Ile ATT	્યનેડ	9 1	ט יט ני	CD LO (
Val	4 E	Arg AGG	Thr ACA	Thr		<b>.</b>
Ile	a) Fig.	er GC	y s GC	A C C	אַנ	ی
Leu TTG		he S IC A	ig t	නය ස	, v.	ب ک
CH		Ph. TT(	Met	Ar	Se	5
TY		Lys	Met ATG	Asp GAC	Tyr Tor	<b>d</b>
70 Asn AAC	Thr ACA	100 Trp TGG	Val GTC	130 Ile ATT	Arg	)
Thr	Ala GCC	Glu GAG	Asp GAT	Ser	Thr ACA	. · · · · · · · · · ·
Thr	Val GTG	G1y GGT	Leu	le TC	Asn J	
Thr	Leu CTG	Val GTG	Thr ]	Ala I GCC A	yr AT	
Gln	Leu	al IG	Val 1 GTC A	Cys A TGT G	H H 5 C D C	
		> છ ച છ			Le	÷
Leu TTG	A D	Glu GAG	110 Phe TTT	Leu CTG	140 Met ATG	
Ala GCT	Ala GCT	Leu CTG	Ile ATC	Asn AAC	Pro	
Lys Ala AAG GCT	Val GTG	Tyr TAC	Asp GAC	Leu CTG	Met	. Y :
Arg Glu GCA GAG	Ala GCT	Val	Cys	Ile	Ala l GCA	1 B
Arg	Leu	Val GTT	His	Ser AGC	Val A	FIG. 1B
			•			

					* *		8,
	Thr	180 Asn AAT 540	Ile	210 11e ATC	n	240 Leu	7
	Phe TTC	Gln CAG	Ser	Tyr	Asn	Pro	
	Ser	Asp	Ser	Val GTC	Val	Thr	
	Leu	Thr ACA	Tyr	Leu CTG	Arg CGG	Lys AAG	
	Val	Asn	Val GTC	Leu CTG	Lys	Leu	
	160 Trp TGG	Asn	190 Val GTG	Thr	220 Arg CGG	Asn	
	Val	Leu	Phe TTT	Val	Arg	Ala GCC	
,	Ile	G1y GGA	Ala GCC	Ile ATC	Lys	Arg AGA	-
	Ala GCC	Phe TTC	Pro	Phe TTC	Arg	Phe	
	Ile	Leu	Asn AAC	Pro	Leu	Ala GCT	
	Met	170 Leu CTG	Ala GCC	200 Val GTG	Val GTC	230 Arg CGA	*
	Val	Pro	Ile	Tyr	Ile	Ser	* * *
·.	Thr	Cys TGC	Ile	Phe	Tyr	Ser	
	Val GT.T	Ser	Cys TGT	Ser TCA	Ile	Arg	FIG. 10
	Arg	Ile ATC	Glu GAG	Val GTC	Lys	Lys	FIG
					:		

## DOGGLASS DEPICT

Leu	270 Pro CCT	<b>ال المالي</b>	300 G1y GGG	900 Ile	ကြောက	060
Met ATG	Ile ATC	His	Asn AAT	Glu		5
Glu GAG	Pro	His	Lys	Phe ITT		
Met	Ser AGC	Ser	G1y GAG	Phe TTC	Leu CTT	
GAA	Tyr	Pro	Pro	Lys AAG	Ser	
250 Leu CTG	Arg	280 Asp GAT	Lys	310 Ala GCC	Thr	
Glu GAG	Thr	Pro	Ala GCC	Ile ATT	Arg CGG	
Gln CAG	Arg AGG	Leu	Pro	Arg	Thr	*
, Ala GCT	Glu GAG	Thr	Ser	Pro	Lys	
Arg CGA	Pro	Leu	Asp GAC	Asn	G1y GGC	
Arg CGC	260 Pro CCC		290 Pro CCT	Val GTC	320 Asn AAT	
Ala GCC	Ser AGC	His	Asn	Ile	Pro	
Asp Ala GAT GCT	Thr	His	Ser AGC	Ala Lys GCC AAG	Met	$\bigcap$
Ast GAT	Ser AGC	Ser	His		Thr	FIG. 1D
Lys	Ser TCA	Pro	Leu CTA	His	Gln CAG	FIG

# 

Gln	360 Pro	œ: д <u>н</u>	60.04	170 Phe TTC	ر 1- ر
Thr	Leu	Asn AAC		l Glu GAG	The
Ala GCC	Tr]	Cys TGC	Tyr	Ile	j C
Lys	Cys TGC	Asp GAT	G1y GGC	Asn	rcrg(
Lys	Ile	Cys	Leu	Phe TTC	TGAGTCTGCCC
340 Glu GAG	Ile ATC	370 His CAC	Trp	400 Thr ACC	415 Cys TGC
Lys	Phe TTC	Ile ATA	Thr ACA	Thr	His
Gln CAG	Val GTG	Asn	Phe TTC	Tyr	Leu
Gln CAG	Gly GGT	Leu	Ala GCC	Ile ATC	Ile ATC
Ser	Leu	Ile	Ser AGC	Ile ATC	Lys
Leu	350 Val GTT	His	380 Tyr TAC	Pro	410 Met ATG
Lys	Ile ATT	Thr	Leu CTC	Asn	Phe TTC
Arg AGA	Ala GCC	Ile ATC	Val GTC	Val	Ala GCC
Arg	Leu	Phe TTC	Pro	Ala GCC	Lys
Ser	Met	Phe TTC	Pro	Ser	Arg
		•	•		

FIG. 1E

TGGCCAGAAAGGCCCAGATGAACTTGGCCTTCTCGACCCTGCAGGCCCTGCAGTGTTA CACAGCAGCTGCTTCCCACCTGCCTATGCAGGCCAGACCTCATCCCTGCAAGCTG GCTTGGCTCGATGCCCCTCTCTGCCCACACCCTCATCCTGCCAGGGTAGGGCCAGGG

AGACTGGTATCTTACCAGCTCTGGGGTTGGACCCATGGCTCAGGGCCAGCTCACAGAGTGC 1502 

TTCCTCTTGGGCACAGAACTAGCTCAGTGGTCGAGCACCCCTGATCGCTGGCTTGGCC

TGGCCCTTGCCTGTGCCGGATCAGGTGGTGGGGGGGGGCGACACGTTCTTACTTT

ATAGGAACCACATAGGAAAGCAGGGAACACGCCCAAGTCCTCCAGGCACATCAGTGTCAGG

**AGACACACATAAACACCAGGTAGCTCCATGGACCCCAGAGAAACTGAGGCTGAAAAĀTC** 

TGTTTTCCACTCCAACTCTGAGTCCCTACTTTTCATAGCCATGGGTATTACTATG

TCCTACCTTGTTATAGTATCCCATGGGGTTTCTGTACCATTTGGGGGAAAAAACTCTA

ATCCTCAAGGCCCCCAAGAGAATCTGTAAGGAGAAAAATAGGCTGATCTCCCTCTACTCT 1978

CCAATCCACTCCACCTTCTTGATATACCTTGGATGTATCCATTCCTCACAGCAAATG

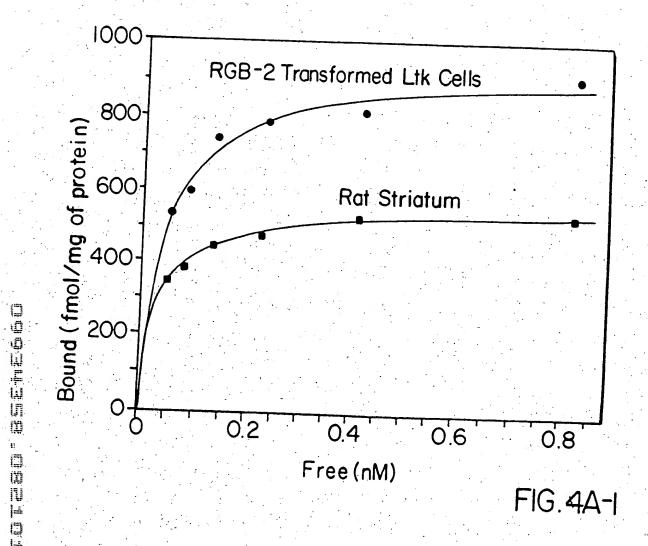
CTGGCCAGTCAGGCCTTGGACCAGTGTTGGAGTTGAAGCTGGATGTGGTAACTTGGGGGCT

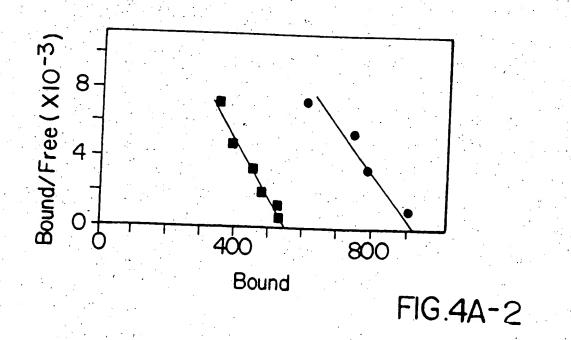
CCTCTGCCTTAGAAGAGGCTGTGGGGTGCTGGGACTGCTGATACCATTGGGCCTGG

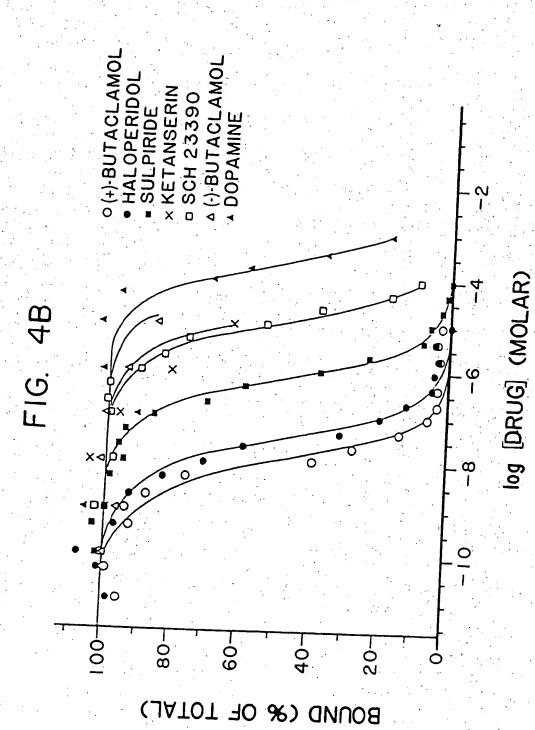
CCCTGAATGAGGGGGAAGCTGCAGTTTGGAGGGTTCTGGGATCCAACTCTGTAACAT

FIG. 1G

	<u>.</u> 6.2		프로 	WPG-(1)
	<b>u.</b>	8 4 H & 1	CRVNIE CRVNIE CRCLOR CFRIPE CRIPE	APERITE SVI
	MISWYDDDLERQNWSRPFNGSEGKADRPHYNYYAMITHEL. IFI IVFGNVLVCMAVSREKALQTHTNY CANDSDFLLTTNGSHV PDHDVTEERDEAWVVGMAITMELL IFI IVFGNVLVCMAVSREKELQTVTNY CANASWNGTEAPG GGARATPYSLQVT LTLVCLAGEL. MLLTVFGNVLVI IAVFTSRAIKAPQNL ONNTTSPPAPFE TGGNTTGISDVTVSYQV. ITSLIJGTH. IFCAVITCNAGVVAAIALERSLONVANY PNITVLAP	USLAMADITIVATI WEWVYLEUWGEWKESRIHCDI FVILDWAMCTASILMLCAISIORYMAVAMPATAYSSKER USLASADILWATI WIPFEASHIMKWAMFGNFWCEFWISIQVLCYTASIETLOMAVORYIMITSBFKYQSLLTKNKA USLASADILWATI WIPFSLANEWMORWEGKTWCEIYLALDWLFCTSSIVHLCAISIORYWSITQAIBYNLKRTPRRI USLAVIDIMUSWLWIBMAALYOMLNNWILGQVTCDLFIALDWLOCTSSILHLCAISIORYWSITQAIBYNNKRTPRRI USLACADILIGIFSMNLYTYYLLMQIMALGTLACDLWIALDYVASNASWASWMILIJSPQRYFSVTRPLESWRAKTRPRRA UNLALADICMAAFNAAFNFVYASHNIMYEGRAFCYFQNLFPITAMFVSIYSMIMILIJSPQRYFMIVRPEOPRISADOMA	TDQNECIIANPAFVVYSSIMSFYVPFIVTLLVYIK INIVLRKRRRVNTKR SGCGGPQPAEPRCEINDQKWYVISSCIGSFFAPOIIMILVYVRIYQIAKRRLQKI SDRSDPDACTISKDMGYTIJYSTFGAFYIPLILMLVLYVRIYQIAKRRTRVP VGERTVLAGQCYIQFLSQPIITFGTAMAAFYLPVTVMCTIYWRIYRETENRAREL TDEGATKCVVAWPEDSGGKMLLYHLIIVIALIYFFI PFIXMACTIYWRIYRETENRAREL	VNPIII YTTENIERNAFWKIIHG VNPIII YCRSP. DFRIA FOETH CL LINPVI YTTENIERRA FWKIII. CR INPVI YAYENKDFONA FWKIII. CR INPVI YAYENKDFONA FWKIIKON INPMCYAL CNKAFRD TFRLILIHGR CWYNPILYCCINHRFRSQERLAPRCC
	EKALO SRAJKO SRAJKO TELLO ORMAN	TII  DEMAFSRIHCDI FVILDWACTASILMLCAISIQRYITAVAMPHIYMTRYSSKR NAMEGKTWCE FWIS JQVLCYTASILMLCAISIQRYITAVAMPHIYMTRYSSKR NAMEGKTWCE IYLALDVLCTSSIVHLCAISIQRYWSITQAIBYNLKRTPRR NAMILGQVICDLFIALDVLOCTSSILHLCAIAIQRYWBITDPIDYVNKRTPRP IMALGTLACDLWLALDVVASNASVMNILIISFQRYFSVTRPLSYRAKTRPRR IMYEGRAFCYFQNLFPITAMFVBIYSMTÄJAAQRYMAIVREFOPRISA	HYPYL VYSRV VYVRI LYGRI LYGRI	ALD THE REAL PROPERTY OF THE R
	ABVSRI FAIAKI FAIAKI FAIALI SEKVNI	VAMEMITSEFFE TTOPITSEFFE TTOPITS VRPFC	TIVE TO THE TANK T	TYCRE CYALE CYALE TYCLE
	RPFNGSEGKADRPHYNYYAMITITELL. IFI IVFGNVLVCMAVSREKALPDHDVTEERDEAWVVGMAITIMENIVEAIVFGNVLVI TATAKFERI SNTTGISDVTVSYQV. ITSLITGTLL. IFCAVITGNAGVVAAITALERSI PWQVA	ARYTAN ARYTAN ARYWSI ARYWAN RYFSU	FIVITE PARTICIPATE	IANA TANA TANA TANA TANA TANA TANA TANA
	I IIVFGI	A PARTY A PART	SFYVP SSIVS SCIGS STFGA TAMAA	VITI VNSA. GNSS. SNST. VNST.
1	SVIVE EFFE FFE FFE FFE FFE FFE FFE FFE FFE	SIL NICOS STEPLOS STATE OF STA	YSSEP AYALES WYVES ICYTES ILTEG	VIT PPVLYSAFTWLGYVNSA PRTIFKFFFWEGYGNSS PTILGAIINWLGYSNSL BETIWELGYWIGYVNST IQQVYLALPWIAMSST
	AMILIA WALLAN VCLAG SLIE STTG	LCVITA LCVITA LCVITA LPCTISI VASNA: TAMFV	VPAFVV SFTNC SINDQK SISKDM ISKDM IFLSQP	LYSAF LEKKF LGAII UWELG
	HYNYY AWVVG LTL QV.IT. ?FIG	VILEPV TSIOV LALDV IALDV NLFPI	SCIIAN KETCCI NEPRCE PDACTI QCXIQ	HEINIHGOCNIFFVLN NEWHVIQDNLIFKEWN YTUTAVGCSWPRTER ALVLPPGESSCHMPTILC VLVSTFCKDCWBETER FEIGTFQEDIYCHKFIQQVY
	KADRP EERDE QVT VIVSY.	HODE FY TOBERY COLF.	CPQPA CPQPA CPQPA CTVLAC	CCN NUL SSC DC
-	NGSEG DHDVT FPYSL FGISD 7A	MFWVVYLEWVGEWKFSRIH VPFGASHIIMKWWNFGNFW IIPFSLANEWNOYWYDGKTW IIEMAALYQWLNNWITLGQVT MNLYTTYLLMQIWALGTLAK AAFNFVYASHNIWYEGRAFK	.QKAI	CWLPFFITHEINIHGOCN. CWLPFFIVNLWHVIQDNL. CWEPFFIVNLWHVIQDNL. CWLPFTIVALVLPPGESSC IWII WILMVLVSTFCKDC. CWLPYHLYFIIGTFQEDIY
	VSRPFI V···PI GGRAC GGNT CGPWQV	H WINNERS	NTD RATH. KGGG. PEDR. YLVGE	TTHETT TVHEY TVALV CYPETI
	SWYDDDLERQNWS SDFLLTTNGSHV. SWNGTEAPGGG, ITSPPAPFETG	VYLEE ASHIJ LANEE ALYOW TTYLL	ISC. PLLFGLNNTD. ISF IPIQMHWYRATH. ISF HPLISIEKKGGG. ISI HPMLGWRTPEDR. LWA. PAILFWQYLVGE LAF. PQCFYSTITTDE	CWLPFFI CWLPFFI CWLPFFI CWLPFFI CWLPFFI CWLPYHL
	YDDDDI VFLLTJ NGTEA SPPAF LAP	WHE SUITE STANKE SWILY		
	A S S S S S S S S S S S S S S S S S S S	HIVATI VMCIA LIVATI I I I I I I I I I I I I I I I I I I I	ALA MAGE	
	PLG. P. C.	IVSLAMADINVATI IDSLACADINMGIA INSLASADILVATI IGSLAVIDIMVSVI LLSLACADILIGI IVVILALADICMAA	TOMIAINWISE AI.IITWWISS LT.SLT.WLIGH LM.IIGLAWLVSE AVI.IAGIWLVSE	KEKKATOMI KEHKALKTI REKRETFUL BERKIVKTI KEKKARTI AKKKFVKTM
	MDFLF MGPFG MGSLQ.FQA.GN MDVLS.FGQ.GN MNTSAPPAVSFN MGACV.VMTDIN	LIVSLAMADII FIDSLAMADII FIVSLASADII LEGSLAVIDIA FLLSLAMADII	ALT. SALT. S	KEKKATOMIAI KERKATUTOT - REKKETTEVIIA - BERKTYKTIOI KEKKAARTIISA - AKKKFVKTMVI
	D <sub>6</sub> β <sub>6</sub> C <sub>2</sub> -21 S <sub>1</sub> S <sub>1</sub>	D <sub>6</sub> β <sub>6</sub> ας <sub>6</sub> G-21 M <sub>1</sub> SK	7 - 7 - 7 - 7 - 7 - 7 - 7 - 7 - 7 - 7 -	72
	_ <b>_                                  </b>	HEOUZO	D & S O Z IV	NA G & S. L. K.

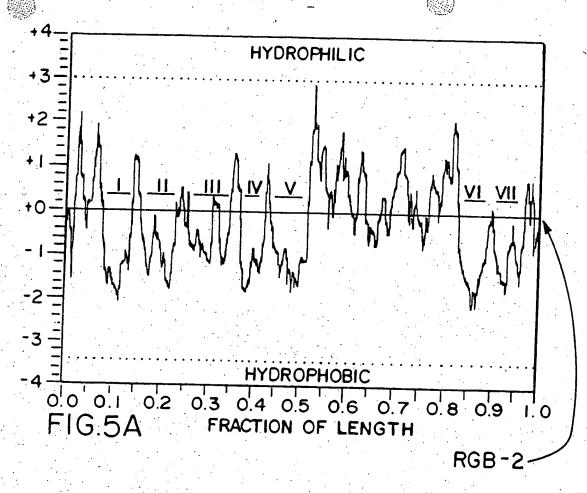


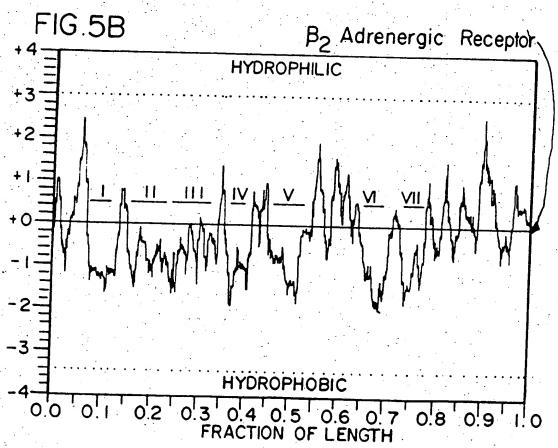




Ki (nM)		Rat Striatum	1.0 >1,000 >1,000 5.3 6,300	67 (87%) >10,000 (13%)	35 (16%) 780 (84%)	27 (25%) >1,000 (75%)	
K	RGB-2	Transformed Ltk-Cells	$\begin{array}{c} 0.83 \\ > 1,000 \\ 3.0 \\ 17,000 \end{array}$		1,000	>1,000	
DRUG			<pre>(+)-Butaclamol (-)-Butaclamol Haloperidol Dopamine + GTP</pre>	Sulpiride high affinity low affinity	SCH 23390 high affinity low affinity	keranserin high affinity low affinity	

FIG. 4C





Econi 2400 nts 2000 0091 1200 800 FIG. 6A Length of DNA: 2477 nts 400 E.co.R. ĸ BamHI Aflil Aflil Asul Asul Avall Avall Avalli Avril Ahal Aatli Apal Acci AccII BamHI AluI BbvI BclI BcnI 

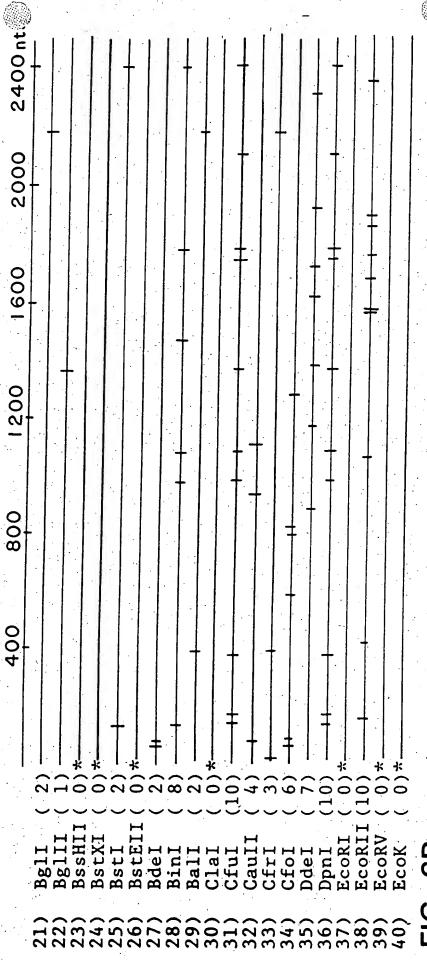


FIG. 6B

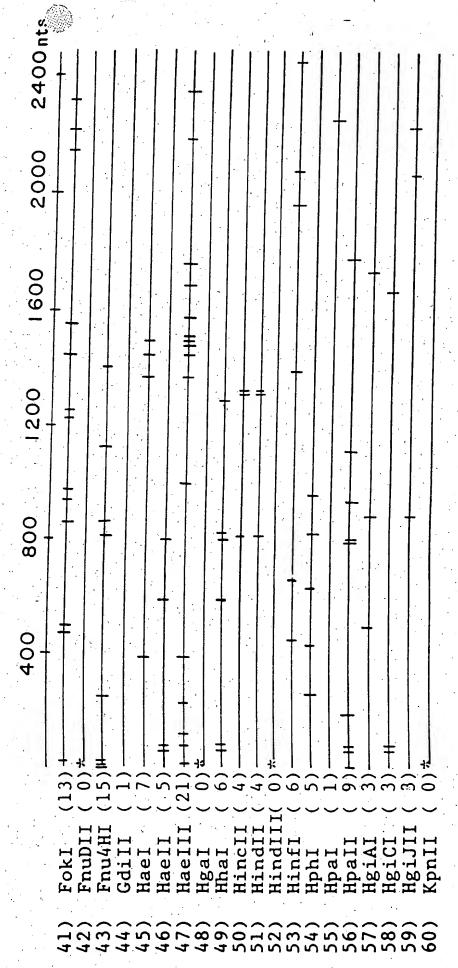
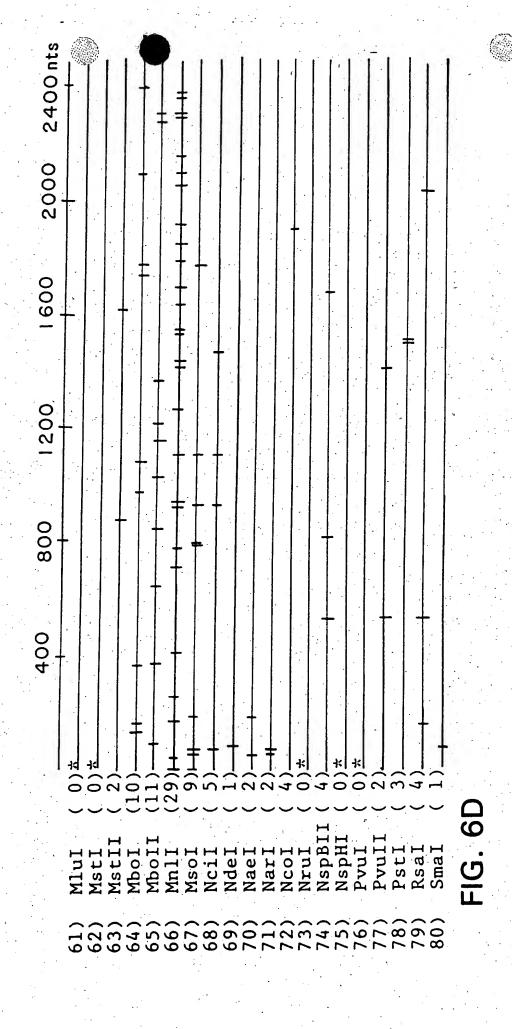
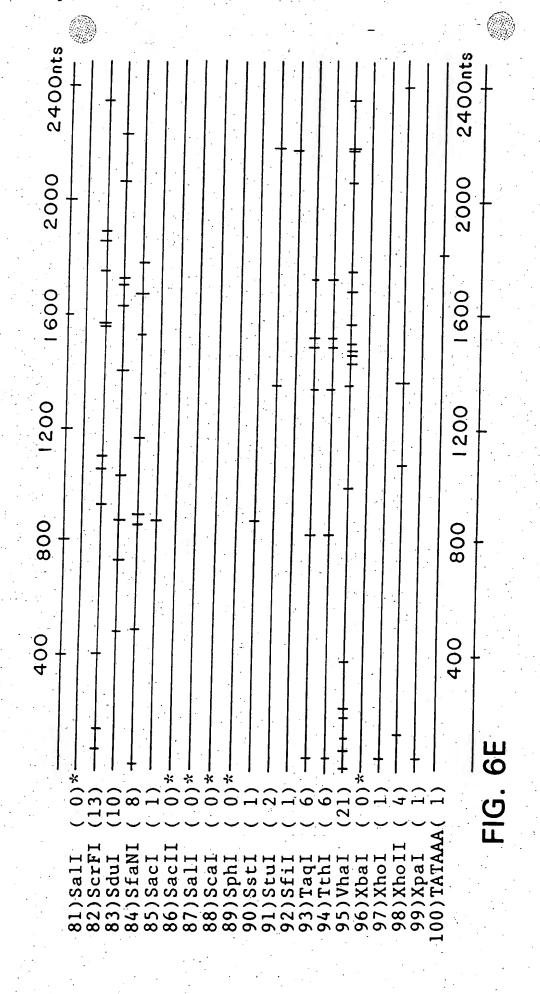


FIG. 6C





### COCHERA DEPICE

### FIG. 7A

GGT GGT CGA 5 CCA CCA GCT 3 Ser Pro Pro Glu Arg Thr Arg Tyr Ser Pro Ile Pro Pro Ser His Gln Leu GTC GGG TGG GCT CTC CTG GGC CAT GTC GGG GTA GGG TGG GTC GGT GGT CGA CAG CCA ACC CAG CCA ACC CAG CCA GCC GTA CAG CCC CAT CCC ACC CAG CCA CCA CCA GCT GIN Pro Thr Arg Glu Asp Pro Val Gln Pro His Pro Thr Gln Pro Pro Ala Pro Ala Thr Thr Ser Ala His Pro Arg Gly Pro Gly Thr Ala Pro Ser His 3'GTC GGG TGG GCT CTC 5'CAG CCC ACC CGA GAG

Thr Leu Pro Asp Pro Ser His His Gly Leu His Ser Thr Pro Asp Ser Pro Ala Leu Ser Pro Thr Arg Pro Thr MET Val Ser Thr Ala Leu Pro Thr Ala Pro Pro 108 GTC GGG GCG Gln Pro Arg 252 222 CAG GGT GTC GTG AGG GCT CCA CAG CAC TCC CGA Ser Pro Arg Pro Val Pro Pro Trp Ser Pro Gln His Ser Arg CTG AGA GGG GCT GGG CAG GGT GGT ACC AGA GAC TCT CCC CGA CCC GTC CCA CCA TGG TCT Asp

Lys Pro Gľu Lys Asn Gly His Ála Lys Árg Thr Thr Pro Árg Ile Ala Lys Ile Asn Gln Arg Arg MET Gly MET Pro Lys Gly Pro Pro Gln Gly Leu Pro Arg Se GTT TGG TCT CTT ACC CGT ACG GTT TTC CTG GTG GGG TTC CTA ACG GTT CTA CAA CAA ACC ACC ACC AAG GAT TGC CAA GAT ACC AGG GAT TGC CAA GAT GAT TGC CAA GAT ACC ACC ACC ACC AAG GAT TGC CAA GAT ACC AAG GAT TGC CAA GAT ACC ACC ACC AAG GAT TGC CAA GAT ACC ACC AAG GAT TGC CAA GAT ACC CAC AAG GAT TGC CAA GAT TGC CA

216 GTA CAT Gln Asp His GTT CTG C Ser Leu Lys Thr GGA Pro JAA ACT CTA GGT CTG GTA CGG GTT ÁCC GTT TTG GGC CTG GAG TT TGA GAT CCA GAC CAT GCC CAA TGG CAA AAC CCG GAC CTC Leu leu . Asp Pro Asp His Ala Gln Trp Gln Asn Pro Asp Leu le Glu Ile Gln Thr MET Pro Ash Cl. T. ... Leu

### DEGLICATE INFILE

TIG. 10. 10. 243

TC GGC ATC CTT C6A G55 GGT CGT CTT CCT CTT TCG GTG AGT CTA CGA GCG

AG CCG TAG GAA G3T C44 CCA GCA GAA GGA GAA AGC CAC TCA GAT GCT CGC

Ju Pro . Glu C TT Pro Ala Glu Gly Glu Ser His Ser Asp Ala Arg

Ser Arg Arg Lys Leu Phe Gln Gln Lys Glu Lys Lys Ala Thr Gln MET Leu Ala

Ala Val Gly Ser Arg Arg Arg Arg Arg Lys Pro Leu Arg Cys Ser Pro Glu Pro

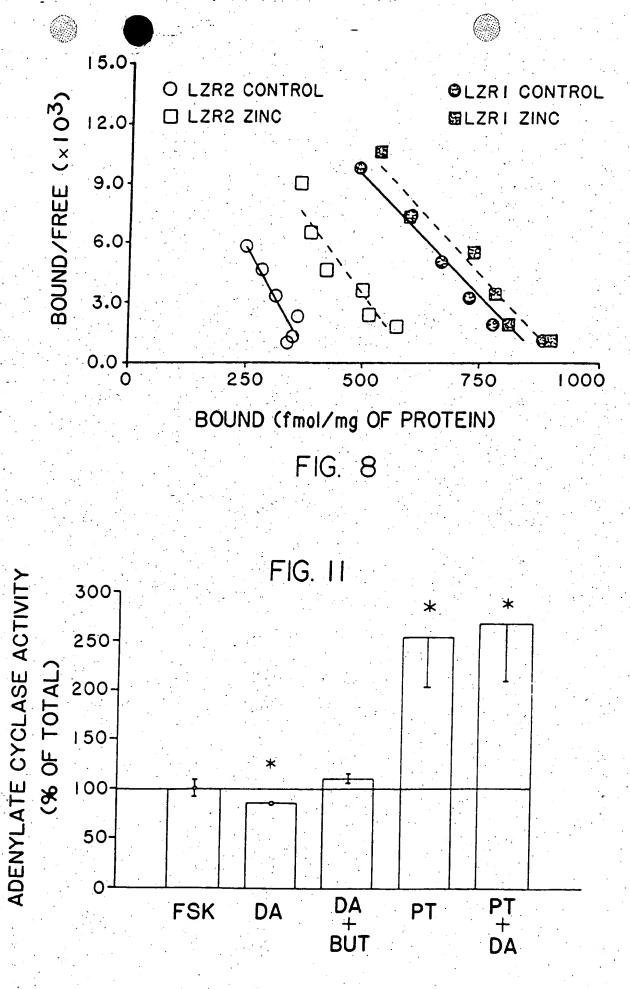
TA 5CA AGA GCC GCA CAA GTA GTA GAC GAC CGA CGG GAA GAA GTA GTG TGT GTA AT 4GT TCT CGG CGT GTT CAT CAT CAT CAT CAT CAT is T Ser Arg Arg Val His His Leu Leu Ala Ala Leu Leu His His Thr His ILE Val Leu Gly Val Phe Ile Ile Cys Trp Leu Pro Phe Phe Ile Thr His Ile Ile Phe Ser Ala Cys Ser Ser Ser Ser Ala Gly Cys Pro Ser Ser Ser His Thr Ser 297 CAT

GA CTT GTA TGT GAC ACT GAC GTT GTA GGG CGG ACA GGA CAT GTC GCG GAA GTG GT GAA CAT CCC GCC TGT CCT GTA CAG CGC CTT CAC TO GIU His Thr Leu . Leu Gln His Pro Ala Cys Pro Val Gln Arg Leu His Leu Asn Ile His Cys Asp Cys Asn Ile Pro Pro Val Leu Tyr Ser Ala Phe Thr Thr Tyr Thr Val Thr Ala Thr Ser Arg Leu Ser Cys Thr Ala Pro Ser Arg Pro

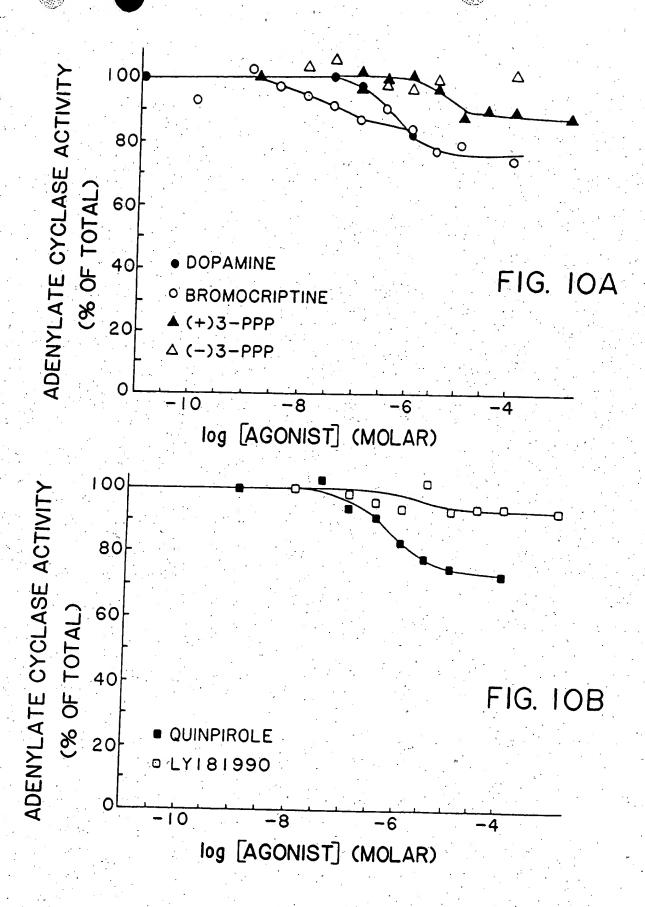
AC CGA CCC GAT ACA GTT GTC GCG GCA CTT GGG GTA GTA GAT GTG GTG GAA GTT TG GCT GGG CTA CAT CTA CAC CAC CTT CAA al Ala Gly Leu Cys Gln Gln Arg Arg Glu Pro His His Leu His Leu Gln Trp Leu Gly Tyr Val Asn Ser Ala Val Asn Pro Ile Ile Tyr Thr Thr Phe Asn Thr Pro Ser Ser Thr Pro Pro Ser Gly Trp Ala MET Ser Thr Ala Pro Val Ala

Arg Ser Ser Thr Ala Asp Ser Ala Ala Cys Ile Glu Phe Arg Lys Ala Phe Leu Lys Ile Leu His Cys STOPLeu Cys Cys Leu Leu Ser Ser Ala Arg Pro Ser . Arg Ser Ser Thr Ala Asp Ser Ala Ala Cy GTA ACT CAA CAT TGA GTT

Arg Thr Ala Ala Cys Phe Pro Pro Pro Cys Pro Val Pro Ala Ser Leu Thr Leu Pro His Ser Ser Leu Leu Pro Thr Ser Leu Pro Ser Ala Gly Gln Pro His Pro CGG CGT GTC GTC GGA CGA AGG GTG GAG GGA CGG GTC ACG GCC GGT CGG AGT GGG GCC GCA CAG CCC GCA CCC TCA CCC AGA CCC AGA CCC AGA CCC AGA CAGA CAGA



DOGENACH DEPICE



03	W.			_					_				
	FSK+DA	23.1	14%	: ·		VIP+DA	2.56	3%			VIP+DA	4.76	
+P.T.		26.7		e A	+P.T.	DA	0.55	<b>%</b> 01	9	+P.T.	DA	0.66	
<b>-1-</b>		G.			+	VIP	2.68	* 1		Ŧ	VIP	5.29	
**	BASAL	1.7				BASAL	0.09	1			BASAL	0.64	
	FSK+DA	14.3 2.1	41%			VIP+DA	0.84	71%			VIP+DA	0.76	
CONTROL		22.6	- · ·	. *	CONTROL	DA	0.32	53%		CONTROL	DA	0.25	
CON	L FSK		-		CON	VIP	2.41			CON	VIP	5	
	BASAL	0.2	1	*	~	BASAL	0.60	-		, T <sub>10</sub>	BASAL	0.78	
		S. E.≍	Ī	*	· ·	· · · · · ·	S.E.	Z				s. E.≺	
	*.	F1G. 12A	÷ a	. ••	•	* *	12B	-	ei 	*		-1G. 12C	
	. <del>.</del>	FIG.					FIG. 12B					FIG.	

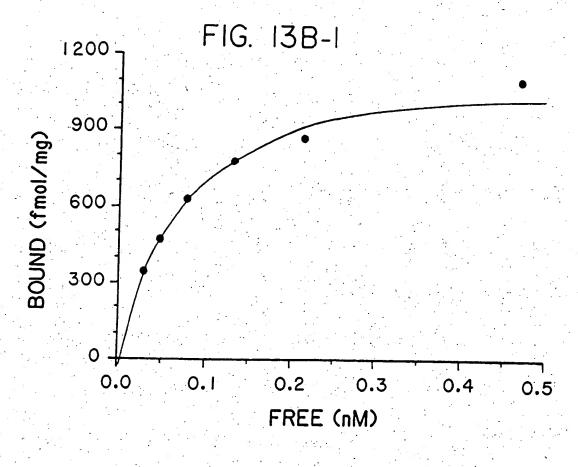
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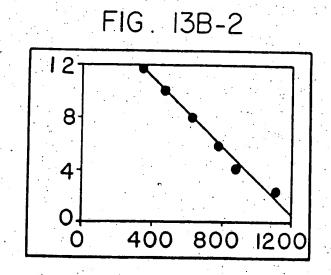
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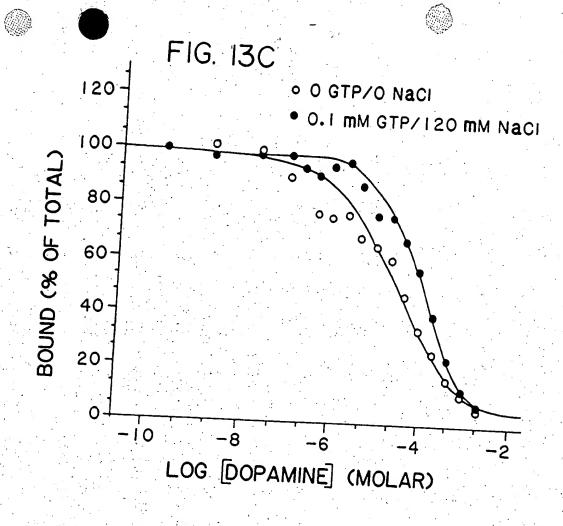
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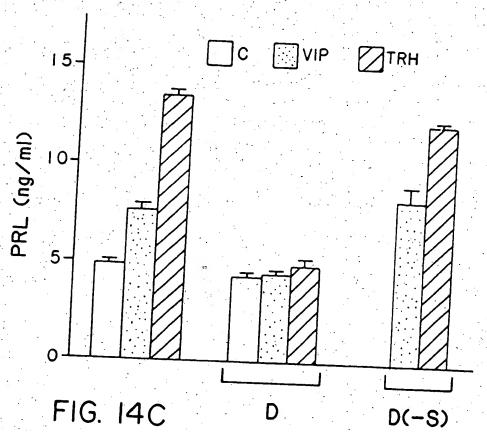
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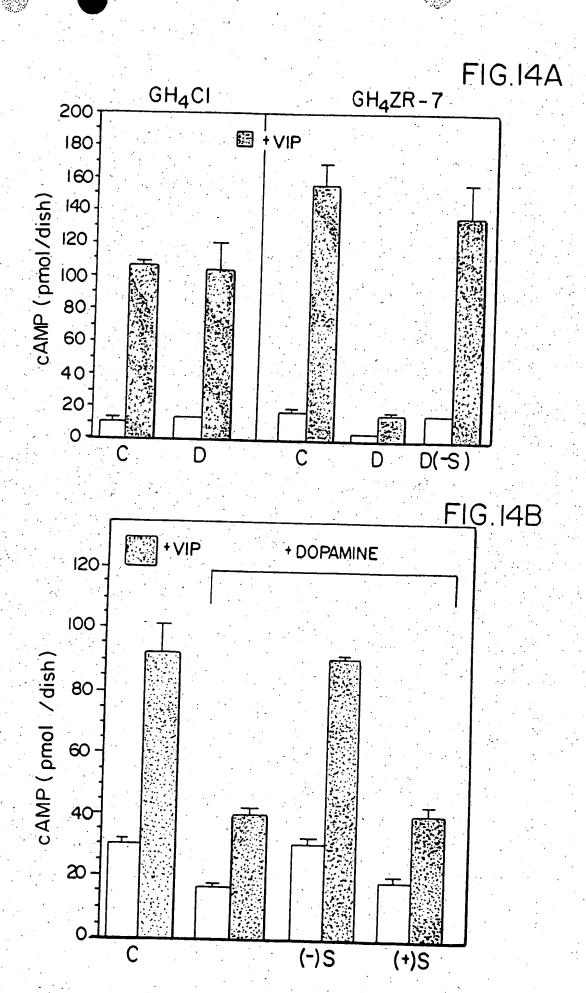
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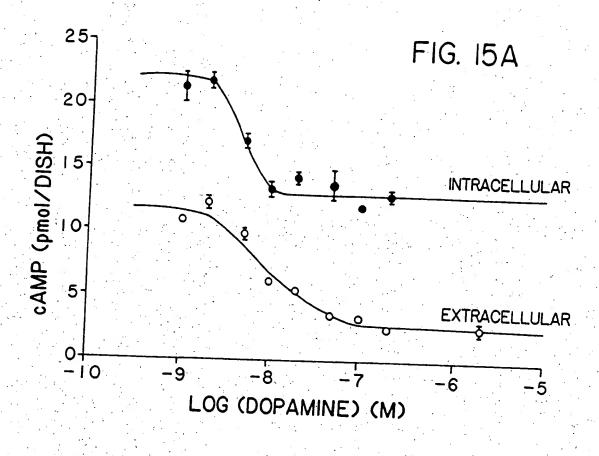


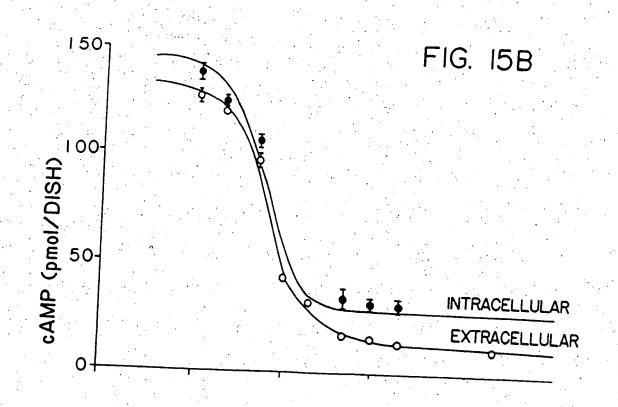


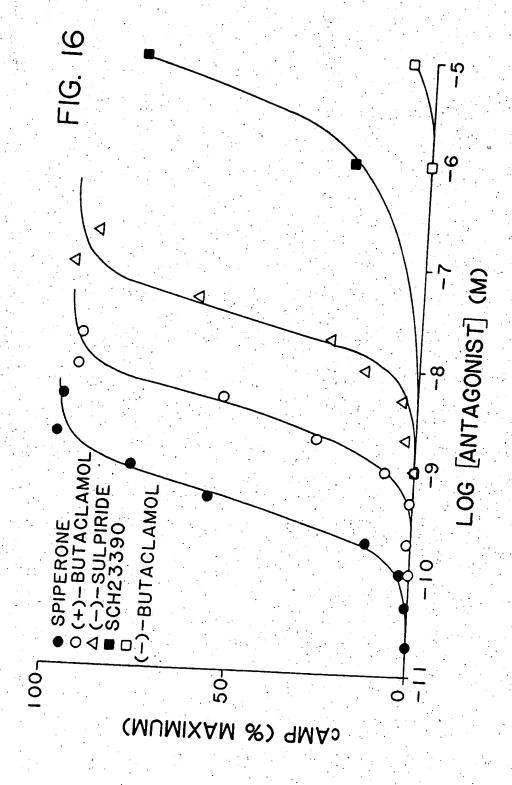


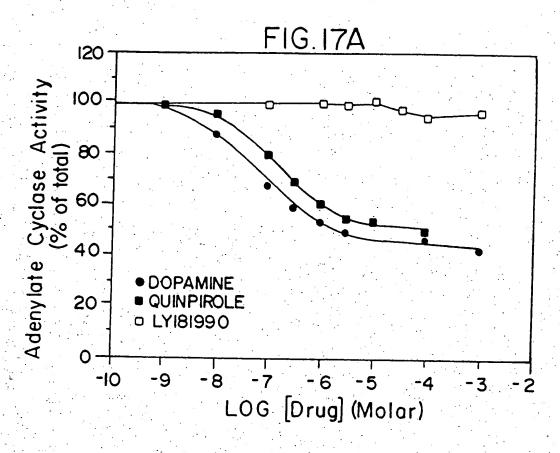


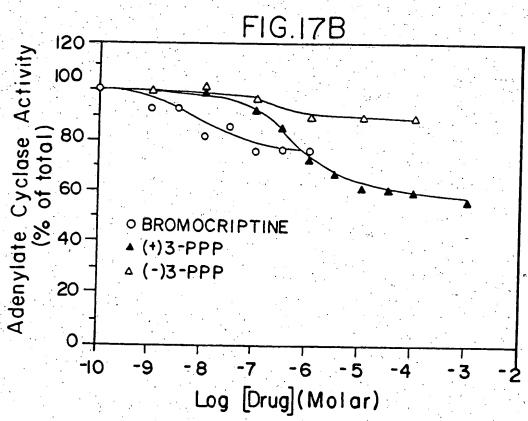












-33 AGAGCCTGGCCACCCAGTGGCTCCACCGCCCTG

 ${\tt METAspProLeuAsnLeuSerTrpTyrAspAspAspLeuGluArgGlnAsnTrpSerArg}$ ATGGATCCACTGAATCTGTCCTGGTATGATGATCTGGAGGCCAGAACTGGAGCCGG ATGGATCCACTGAACCTGTCCTGGTACGATGACGATCTGGAGGCGGGG 

ProPheAsnGlySerAspGlyLysAlaAspArgProHisTyrAsnTyrTyrAlaThrLeu

CCCTTCAACGGGTCAGACGGGGGGGGGGGCGCCCCCCTACAACTACTATGCCACACTG CCCTTCAATGGGTCAGAAGGGAAGGCAGACAGGCCCCACTACAACTACTATGCCTG

FIG. 18A

 $\underline{LeuThrLeuLeuLleAlaValIleValPheGlyAsnValLeuValCysMETAlaValSer}$ CTCACCCTGCTCATCGTCATCGTCTTCGGCAACGTGCTGTGCATGGCTGTGTCC CTCACCCTCCTCATCTTATCATCGTCTTTGGCAATGTGCTGTGTGCATGGCTGTATCC Phelle

ArgGluLysAlaLeuGlnThrThrAsnTyrLeuIleValSerLeuAlaValAlaAsp CGCGAGAGGCGCTGCAGACCACCACTACCTGATCGTCAGCCTCGCAGTGGCCGAC CGAGAGAAGGCTTTGCAGACCACCACTACTTGATAGTCAGCCTTGCTGTGGCTGAT

LeuLeuValAlaThrLeuValMETProTrpValValTyrLeuGluValVal GlyGluTrp

CTTCTGGTGGCCACACTGGTAATGCCGTGGGTTGTCTACCTGGAGGTGGTGGTGAGTGG

FIG. 18B

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**AAATTCAGCAGGATTCACTGTGACATCTTCGTCACTCTGGACGTCATGATGTGCACGCCG** AAATTCAGCAGGATTCACTGTGACATCTTTGTCACTCTGGATGTCATGATGTGCACAGCA

AGCATCCTGAACTTGTGTGCCATCAGCATCGACAGGTACACAGCTGTGGCCATGCCCATG SerIleLeuAsnLeuCysAlaIleSerIleAspArgTyrThrAlaValAlaMETProMET AGCATCCTGAACCTGTGTGCCATCAGCATTGACAGGTACACAGCTGTGGCAATGCCCATG LeuTyrAsnThrArgTyrSerSerLysArgArgValThrValMETIleSerIleValTrp

CTGTACAATACGCGCTACAGCTCCAAGCGCCGGGTCACCGTCATGATCTCCATCGTCTGG CTGTATAACACGCCTACAGCTCCAAGCGCCGAGTTACTGTCATGATTGCCATTGTCTGG

FIG. 18C

480

ValLeuSerPheThrIleSerCysProLeuLeuPheGlyLeuAsnAsnAlaAspGlnAsn

200  ${\tt GluCysIleIleAlaAsn} \overline{\tt ProAlaPheValValTyrSerSerIleValSerPheTyrVal}$ 

GAGTGCATCATTGCCAACCCGGCCTTCGTGGTCTACTCCTCCATCGTCTCTTCTACGTG GAGTGTATCATTGCCAACCCTGCCTTTGTGGTCTACTCCTCCATTGTCTCATTCTACGTG

ProPhelleValThrLeuLeuValTyrIleLysIleTyrIleValLeuArgArgArg

FIG. 18D

=	FIG. 18F
840	GGGAGTTTCCCAGTGAACAGGCGGGGAGCTGCCCGGCGAGCCCAGGAGCTGGAG  11 111111 11111 111111  CATGCTGCCGCCGAGCTGGAG  ASD
	270 GlySerPheProValAsnArgArgArgValGluAlaAlaArgArgAlaGlnGluLeuGlu
s-	AAG
	AAGGCCAACTGTACTCACCCCGAGGACATGAAACTCTGCACCGTTATCATGAAGTCTAAT
	* LysGlyAsnCysThrHisProGluAspMETLysLeuCysThrVallleMETLysSerAsn
720	AAGCGAGTCAACACCCAAACGCAGCCGAGCTTTCAGGGCCCACCTGAGGGCTCCACTA
(i)	240 LysArgValAsnThrLysArgSerSerArgAlaPheArgAlaHisLeuArgAlaProLeu

 ${\tt METG1uMETLeuSerSerThrSerProProG1uArgThrArgTyrSerProI1eProPro}$ 

 ${\bf Ser His His Gln Leu Thr Leu Pro Asp Pro Ser His His Gly Leu His Ser Thr Pro Asp}$ 

AspHisProLysIleAlaLys SerProAlaLysProGluLysAsnGlyHisAlaLys

· GACCACCCCAAGATTGCCAAG **AGTCCTGCCAAACCAGAAGAATGGGCACGCCAAGATTGTCAATCCCAGGATTGCCAAG** AGCCCCCCCAAACCAGAGAAGAATGGGCATGCCAAA..

FIG. 18F

IleValAsn

096

.

 $Ile Phe {\tt GluIleGlnThrMETProAsnGlyLysThrArgThrSerLeuLysThrMETSer}$ 

TTCTTTGAGATCCAGACCATGCCCAATGGCAAAACCCGGGACCTCCCTTAAGACGATGAGC

ArgArgLysLeuSerGlnGlnLysGluLysLysAlaThrGlnMETLeuAlaIleValLeu

**CGCAGAAAGCTCTCCCAGCAGAAGGAGAAAAGCCACTCAGATGCTTGCCATTGTTCTC** 

399 GlyValPhellelleCysTrOLeuProPhePhelleThrHislleLeuAsnIleHisCys

**GGCGTGTTCATCATCTGCTGCCTTCTTCATCACACACATCCTGAACATACACTGT** GCCGTCAACCCCATCATCTACACCCTTCAACATCGAGTTCCGCAAGGCCTTCATGAAG

607

**AspCysAsnIleProProValLeuTyrSerAlaPhéThrTrpLeuGlyTyrValAsnSer** 

GACTGCAACATCCCGCCTGTCCTGTACAGCGCCTTCACGTGGCTGGGCTATGTCAACAGC GATTGCAACATCCCAGTCCTCTACAGCGCCTTCACATGCCTGGGCTATGTCAACAGT 

AlaValAsnProllelleTyrThrThrPheAsnIleGluPheArgLysAlaPheLeuLys

GCCGTCAACCCCATCATCTACACCACCTTCAACATCGAGTTCCGCAAGGCCTTCATGAAG IleLeuHisCys \*

**ATCCTCCACTGCTGCTGCCTGCCGCACAGCCTGCTTCCCACCTCCCTGCC** 

ATCTTGCACTGCTGA

FIG. 18H

## HOTUS BULLEGO

CAGGCCGGCCAGCCTCACCCTTGCGAACCGTGAGGCAAGGCCTGGGTGGATCGGCCTC 1437

CTCTTCTTAGCCCCGGCAGGCCCTGCAGTGTTCGCTTGGCTCCATGCTCCTCACTGCCCG

CACACCCTCACTCTGCCAGGGCAGTGCTAGTGAGCTGGGCATGGTACCAGCCCTGGGGGT

GGCCCCAGCTCAGGGGCAGCTCATAGAGTCCCCCCTCCCACCTCCAGTCCCCCTATCCTT

GGCACCAAAGATGCAGCCGCCTTCCTTGACCTTCCTCTGGGGCTCTAGGGTTGCTGGAGC 1677

CTGAGTCAGGGCCCAGAGGCTGAGTTTTCTCTTTGTGGGGCTTGGCGTGGAGCAGGCGGT

GGGGAGAGATGGACAGTTCACACCCTGCAAGGCCCACAGGAAGGCAAGCTCTTTGC 1797

CGAGGAGCCAGGCAACTTCAGTCCTGGGAGCCCCATGTAAATACCAGACTGCAGGTTGGA

## DOGUES DEFIN

CTTTCCAGGCTAGTCCGGACCCACCTCACCCCGTTACAGCTCCCCCAAGTGGTTTCCACAT

GCTCTGAGAAGAGGCCCTCATCTTGAAGGGCCCAGGAGGGTCTATGGGGAGAGGAACT 2037

CCTTGGCCTAGCCCACCCTGCCTTCTGACGGCCCTGCAATGTATCCCTTCTCACAGC

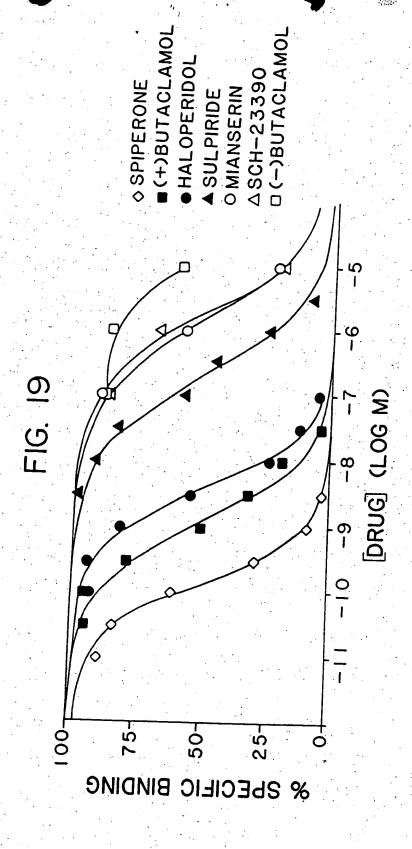
ACATGCTGGCCAGCCTGGCAGGGAGGTCAGGCCCTGGAACTCTATCTGGGCCT 2157

GGGCTAGGGACATCAGAGGTTCTTTGAGGGACTGCCTCTGCCACACTCTGACGCAAAACC

CTCTGCCTTAGAGGCCCCACGGCTAAGAGGCTGCTGAAAACCATCTGGCCTGGCCTGGC

CCTGCCCTGAGGAGGGGCAAGCTGCAGCTTGGGAGGCCCCTGGGGCCTAGACTCTG 2397

TAACATCACTATCCGATGCACCAAACTAAAAACTTTGACGAGTCACCTTC (A)<sub>n</sub> 2449



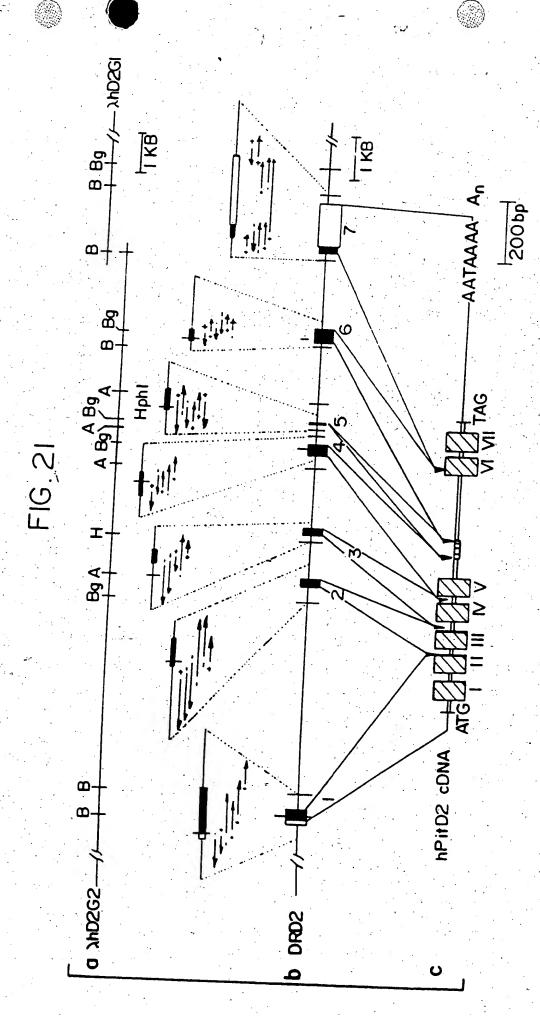
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6.0 4.0

2.0

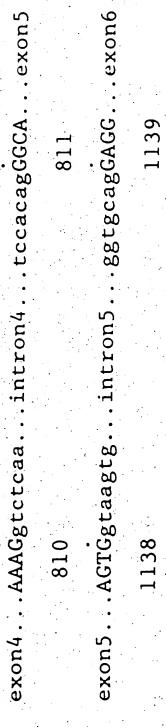
1.6

1.0



DRUG HUMAN [	HUMAN D <sub>2</sub> RAT D <sub>2</sub>	RAT STRIATUM
SPIPERONE 0.125	0.35	0.56
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JOL	. <u>.</u> .	ο α - ιτ
20	160	205
MIANSERIN (5-HT) 2685	4300	4600
SCH 23390 (DI) 2145	2500	0025
<u></u>	00001	00001
Kd [3H] DOMPERIDONE 0.74	0.40	
	2	010

*	.exon2		.exon3	*	.exon4	*
286	.tccccagGTGG	396	.cttgcagGTAC	533	.ccccagACCA	724
	intronl		intron2		intron3	
2851	1GGAGgtaggtgintronl	395	2ACAGgtgagcc.	532	3GCAGgtacatt.	723
23	exon.		exon2		exon3	



GCGTexon7	 3 1 1 1 1
n6ccccagGCGT.	450 5: 10 10 10 10 10 10 10 10 10 10 10 10 10
tcintron6.	. 4
CTCGgtgagtc	hegine with
exon6CT	lNumberino

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